

IDENTIFIERS

dbEST Id: 1036015
 EST name: 26078
 GenBank Acc: AA394495
 GenBank gi: 2047706

CLONE INFO

Clone Id: 129022XP (3')
 DNA type: cDNA

PRIMERS

Sequencing: M13 -21 dye primer
 PolyA Tail: Unknown

SEQUENCE

AAGANTGNGGCCCCAGGGCTGNGCTCCNNGTCCNCGGGTCCCCCTTCAACATTGTACANG
 GCCCATNCNCTNCCGGGTTCCCCAATGGCTAGGATCAACCACCGCTACTCAGNCCNNTGC
 AGGATATGTTTCCNCGCTGTGCTGCTCTAATCATGACTAATTGGGCTCTTGGAAGCA
 CAGCCGCTCTGAGAAAGATATTGTATGGAAAAGATGGAAAGCCAAAGTATCCCAAGAAGAT
 GGGTGATACTTCCTCCATTCCTTTAGAAGCCATTGTTGCTTATCAGTAAAAGCTCTTAAT
 AAAGCTGAAAATGAGACTTTCTTTGGGTTCTCTGNNNCGTTNCCNTTTTTGTTGCGTCTA
 TGTATGGTTATAACATGTTTATTCCTTTTGTTCATATGTTTTGATTTTGAAGTTAG
 AGAGATTTAGAAATGTACTTGTGTAGTTGTTTCTCACGCAAACCAATTCCTCTTTATGTA
 TCGCATACATGAGTCAATAATAAATATGATTACTNGT

Entry Created: Apr 25 1997
 Last Updated: Oct 30 1997

LIBRARY

dbEST lib id: 71
 Lib Name: Lambda-PRL2
 Organism: Arabidopsis thaliana
 Strain: var columbia
 Vector: lambda Zip-Lox
 R. Site 1: Sal
 R. Site 2: Not
 Description: Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA.

SUBMITTER

Name: Thomas Newman
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 Institution: Michigan State University
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 , E. Lansing, Mi
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 E-mail: 22313tcn@ibm.cl.msu.edu

CITATIONS

Medline UID: 95148729
 Title: Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones
 Authors: Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E., Somerville, C.
 Citation: Plant Physiol. 106: 1241-1255 1994

MAP DATA

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IDENTIFIERS

dbEST Id: 1456547
 EST name: 499
 GenBank Acc: AA739734
 GenBank gi: 2778285

CLONE INFO

Clone Id: 8812M (3')
 DNA type: cDNA

PRIMERS

Sequencing: M13_Universal
 PolyA Tail: Unknown

SEQUENCE

GGGTACAGCATCCACAGGGAGGGCTGTTTGAATTTGIGGTCTGTCCGCATTACCTTTTC
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 AAGAAGTTTGAGGGTTTCCCCTCCAATAGAAAGGCTTTGATACCTTTCCTATTGTGAGAG
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 GTGATTACTCTTCAATGGAACCCTTACAAATACATTTAATTGCTTTCCT

Entry Created: Jan 15 1998
 Last Updated: Jan 15 1998

COMMENTS

The sequence entry for this EST has been reverse
 complimented and is being submitted in the sense
 orientation.

LIBRARY

dbEST lib id: 1071
 Lib Name: PtIFG2
 Organism: Pinus taeda
 Tissue type: xylem
 Vector: lambda ZAP
 R. Site 1: EcoRI
 R. Site 2: XhoI
 Description: The tissue source for this library is xylem. The xylem
 tissue was harvested in spring and summer from branches of
 seed orchard trees which are clones of the same genotype.
 Branches were 4-6 inches in diameter. The cDNAs were
 directionally cloned into Lambda Zap and were rescued as a
 Bluescript derivative in the EcoRI and XhoI sites.

SUBMITTER

Name: Claire S. Kinlaw
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 , Berkely, CA 94701
 Tel: 5105596429
 Fax: 5105596440
 E-mail: csk@s27w007.pswfs.gov

CITATIONS

Title: Loblolly pine cDNAs
 Authors: Kinlaw, C.S.
 Year: 1995
 Status: Unpublished

MAP DATA

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IDENTIFIERS

dbEST Id: 2304763
 EST name: EST241799
 GenBank Acc: AI491090
 GenBank gi: 4386400

CLONE INFO

Clone Id: cLEB1E14
 Source: Clemson University Genomics Institute
 DNA type: cDNA

PRIMERS

PolyA Tail: Unknown

SEQUENCE

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 TCGTCGAGGATACTTTGGTCTTCCTTCTTCCATCAAAGAGCTTCTTCAGACGACGATG
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 TTTGTAACC

Entry Created: Mar 8 1999

Last Updated: May 18 2001

PUTATIVE ID Assigned by submitter
 synaptic glycoprotein (SC2)

LIBRARY

dbEST lib id: 1648
 Lib Name: tomato shoot, Cornell
 Organism: Lycopersicon esculentum
 Cultivar: TA496
 Tissue type: shoot meristem
 Develop. stage: 8 week old plants
 Lab host: XL0LR
 Vector: pBK_CMV
 R. Site 1: EcoR1
 R. Site 2: Xho1
 Description: cLEB - Tomato Shoot Meristem EST Library. Oligo-dT primed
 cDNA library made from tomato vegetative shoots including
 meristems and small expanding leaves.

SUBMITTER

Name: CUGI
 Lab: Clemson University Genomics Institute
 Institution: Clemson University
 Address: 100 Jordan Hall, Clemson, SC 29634, USA
 E-mail: <http://www.genome.clemson.edu/orders/index.html>

CITATIONS

Title: Generation of ESTs from tomato shoot meristem
 Authors: van der Hoeven,R.S., Matern,A.L., Vision,T., Holt,I.E.,
 Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y.,
 Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin
 ,G.B., Giovannoni,J.J., Tanksley,S.D.
 Year: 1999
 Status: Unpublished

MAP DATA

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IDENTIFIERS

dbEST Id: 2949724
 EST name: 603012D11.x1
 GenBank Acc: AI861123
 GenBank gi: 5525284

CLONE INFO

Plate: 603012 Row: D Column: 11
 DNA type: cDNA

PRIMERS

PolyA Tail: Unknown

SEQUENCE

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 CACTG

Entry Created: Jul 19 1999
 Last Updated: Jul 19 1999

LIBRARY

dbEST lib id: 1732
 Lib Name: 603 - stressed root cDNA library from Wang/Bohnert lab
 Organism: Zea mays
 Cultivar: B73
 Organ: root
 Tissue type: seedling
 Develop. stage: salt stress
 Lab host: E. coli XL Gold
 Vector: pBluescriptII SK(+) XR
 Description: Seedling stressed root cDNA library from Wang/Bohnert lab

SUBMITTER

Name: Walbot V
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 Fax: 650 725 8221
 E-mail: walbot@stanford.edu

CITATIONS

Title: Maize ESTs from various cDNA libraries sequenced at Stanford University.
 Authors: Walbot, V.
 Year: 1999
 Status: Unpublished

MAP DATA

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LOCUS ATT22E16 103240 bp DNA linear PLN 23-FEB-2000
 DEFINITION Arabidopsis thaliana DNA chromosome 3, BAC clone T22E16.
 ACCESSION AL132975
 VERSION AL132975.1 GI:6434228
 KEYWORDS .
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1
 AUTHORS Benes,V., Wurmbach,E., Drzonek,H., Ansorge,W., Mewes,H.W.,
 Lemcke,K., Mayer,K.F.X., Quetier,F. and Salanoubat,M.
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 103240)
 AUTHORS EU Arabidopsis sequencing,project.
 TITLE Direct Submission
 JOURNAL Submitted (23-FEB-2000) MIPS, at the Max-Planck-Institut fuer
 Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
 lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project
 Coordinator: Marcel Salanoubat and Francis Quetier, Groupement
 d'Interet Public, Centre National de Sequencage - GENOSCOPE; 2 rue
 Gaston Cremieux, BP191, 91006 Evry Cedex, France;
 http://www.genoscope.cns.fr
 COMMENT Information on performance of analysis and a more detailed
 annotation of this entry and other sequences of chromosomes 3, 4
 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
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 /variety="Columbia"
 /db_xref="taxon:3702"
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 CDS complement(join(3660..3728,3821..4575,5038..5077,
 5262..5330))
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PIGNVFRNCAYWSFGAYIAYYNHPLYTPVSDLQMKIGFGFGLVCQVANFYCHILLK
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exon      complement(3821..4575)
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exon      complement(5038..5077)
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          /number=3
intron    complement(5078..5261)
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          /number=3
exon      complement(5262..5330)
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CDS       join(10334..11042,11136..11350)
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CDS       join(13994..14039,14159..14261,14513..14610,14695..14795,
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exon      14159..14261

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/ number=3
intron 14611..14694
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exon 14695..14795
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/ number=4
intron 14796..15213
/ gene="T22E16.40"
/ number=4
exon 15214..15369
/ gene="T22E16.40"
/ number=5
gene 17259..18094
/ gene="T22E16.50"
CDS join(17259..17479,17564..17699,17867..18094)
/ gene="T22E16.50"
/ note="similarity to MtN24, Medicago truncatula,
EMBL:MTY15290
Contains Prokaryotic membrane lipoprotein lipid attachment
site AA164-174"
/ codon_start=1
/ product="putative protein"
/ protein_id="CAB75897.1"
/ db_xref="GI:7076782"
/ translation="MRSPHAFRNGESPTLRDHTHFHSTVTAQKLRRFNSLILLLRLAS
FSFSLASAVFMLTNSRGSSASPHWYDFDAFRFVFVANAIVALYSVFEMGTCVWEFSRET
TLWPEAFQVWFDFGHQVFSYLLLSAGSAAAALARTMRGGDTCTANKAFCLQSDVAIG
LGFAAFLLFLAFSSCFSGFRVACFLITGSRFHLYS"
exon 17259..17479
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/ number=1
intron 17480..17563
/ gene="T22E16.50"
/ number=1
exon 17564..17699
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/ number=2
intron 17700..17866
/ gene="T22E16.50"
/ number=2
exon 17867..18094
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/ number=3
gene 18283..21473
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gene complement(join(18283..18465,18558..18686,18800..18955,
19051..19166,19272..19452,19597..19695,19991..20084,
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19051..19166,19272..19452,19597..19695,19991..20084,
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/ codon_start=1
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/ protein_id="CAB75898.1"
/ db_xref="GI:7076783"
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VARKEENYFFALSKYQKPLEDILAQNPFRVQPSYRLNEVQSWIKSGLRDFSISRALVD
WGIPVPDDDKQTIYVWFDALLGYISALTEDNKQQLLETAVSFGWPASLHLIGKDILRF
HAVYWPAMLSAGLELPKMVFGHGFLTKDGMKMGKSLGNTLEPFELVQKFGPDVARYF
FLREVEFGNDGDYSEDRFIKIVNAHLANTIGNLLNRTLGLLKKNCSTLVVDSTVAAE
GVPLKDTVEKLVEKARTNYENLSLSSACEAVLEIGNAGNTYMDQRAPWFLFKQGGVSA
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exon      complement(20260..20384)
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intron    complement(20385..20535)
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CDS       join(24371..25918,26038..26264,26340..26672,26901..27147,
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LREKIETPTPWRYNRERREVI LDR LAWSTQFENFLATKWTTAKRFGLEGGESLI PGMK
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intron    26673..26900
           /gene="T22E16.70"
           /number=3
exon      26901..27147
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intron    27148..27247
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           /number=4
exon      27248..27376
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intron    27377..27461
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           /number=5
exon      27462..27677
           /gene="T22E16.70"
           /number=6
intron    27678..27763
           /gene="T22E16.70"
           /number=6
exon      27764..27887
           /gene="T22E16.70"
           /number=7
intron    27888..27996
           /gene="T22E16.70"
           /number=7
exon      27997..28202
           /gene="T22E16.70"
           /number=8
gene      30394..31044
           /gene="T22E16.80"
CDS       30394..31044
           /gene="T22E16.80"
           /codon_start=1
           /product="putative protein"
           /protein_id="CAB75900.1"
           /db_xref="GI:7076785"
           /translation="MAEKEKKT KKKKKKEKHQSSDISFKPSSDVKGLKFGGQIIVKSF
TIRRARTFELLKLLSLPSSSSPPLLSTAAYLPTNFTILAHHAHWTLLTGLGTRKSKVV
VFVFETEAMKSSVVAEEGGIWPSEIPLGDVNKKMIRKLNWEMARFKFRKGCITFYVY

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AVRNAGNEGFAAAEDLKVILQAVVALKDFMDHTAMLVMPHQKSINYSSCPPFAMAH"
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gene      32280..34478
          /gene="T22E16.90"
gene      complement(join(32280..33167,34017..34478))
          /gene="T22E16.90"
CDS       complement(join(32280..33167,34017..34478))
          /gene="T22E16.90"
          /note="strong similarity to probable beta-1, 3-glucanase,
          Triticum aestivum, PIR:T06268"
          /codon_start=1
          /product="beta-1, 3-glucanase-like protein"
          /protein_id="CAB75901.1"
          /db_xref="GI:7076786"
          /translation="MAKAPPSISLLLLLCAAVFLTIPAVISAGVNYGTGLNLPPTQ
          VANFIKTQTSIDSVKIFDVNPDILRAFAGTGISVVTVPNGDIPALANGRQARRWVS
          NILPFHPQTKIKYISVGNEILLTGDNNMINLLPAMRNLLNALVRAGVRDVKVTTHS
          LNIIAYDLTGAPSSGRFRPGWDKGILAPILAYHRRTKSPFMVNPYPYFGFDPKNVNF
          IFRTPYKAVRDPFTRHVYTNMFDALMDSTYSAMKALGYGDVNIIVVGETGWPSACDAP
          W CSPANAAWFNLNIIKRAQQGTPLMPNRRFETYIFGLFNEEGKPGPTAERNWGLFRAD
          FSPVYDVGLLRNGQGGGRPALPAPSTAGGKWCVARSGATNTQLQDSINWVCGQGVDC
          KPIQAGGSCFNPPSSLRTHASFVMNAYFQSHGRTDGACNFSGTGMIVGNPNPNSGACKY"
exon      complement(32280..33167)
          /gene="T22E16.90"
          /number=1
intron    complement(33168..34016)
          /gene="T22E16.90"
          /number=1
exon      complement(34017..34478)
          /gene="T22E16.90"
          /number=2
gene      36268..38552
          /gene="T22E16.100"
CDS       join(36268..36306,36634..36709,37000..37123,37468..37552,
          37647..37779,37958..38052,38163..38241,38328..38410,
          38502..38552)
          /gene="T22E16.100"
          /note="Contains Triosephosphate isomerase active site
          AA164-174"
          /codon_start=1
          /product="cytosolic triosephosphatisomerase"
          /protein_id="CAB75902.1"
          /db_xref="GI:7076787"
          /translation="MARKFFVGGNWKCNGTAEVKKIVNTLNEAQVPSQDVVEVVVSP
          PYVFLPLVKSTLRSDFFVAAQNCWVKKGGAFTGEVSAEMLVNLDIPWVILGHSERRAI
          LNESSEFVGDKVAYALAQGLKVIACVGETLEEREAGSTMVDVAAQTKAIDRVTNWSN
          VVIAYEPVWAIGTGKVASPAQAEVHDELKRWLAKNVSADVAATTRIIYGGSVNGGNC
          KELGGQADV DGLVGGASLKPEFIDI I KAAEVK KSA"
exon      36268..36306
          /gene="T22E16.100"
          /number=1
intron    36307..36633
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          /number=1
exon      36634..36709
          /gene="T22E16.100"
          /number=2
intron    36710..36999
          /gene="T22E16.100"
          /number=2
exon      37000..37123
          /gene="T22E16.100"
          /number=3
intron    37124..37467
          /gene="T22E16.100"
          /number=3
exon      37468..37552
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intron    37553..37646
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          /number=4
exon      37647..37779

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/ gene="T22E16.100"
/ number=5
intron 37780..37957
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/ number=5
exon 37958..38052
/ gene="T22E16.100"
/ number=6
intron 38053..38162
/ gene="T22E16.100"
/ number=6
exon 38163..38241
/ gene="T22E16.100"
/ number=7
intron 38242..38327
/ gene="T22E16.100"
/ number=7
exon 38328..38410
/ gene="T22E16.100"
/ number=8
intron 38411..38501
/ gene="T22E16.100"
/ number=8
exon 38502..38552
/ gene="T22E16.100"
/ number=9
gene 40736..42437
/ gene="T22E16.110"
CDS join(40736..40780,40868..41170,41263..41398,41477..41622,
41702..41825,42013..42437)
/ gene="T22E16.110"
/ note="strong similarity to serine/threonine-specific
protein kinase NAK, Arabidopsis thaliana, PIR:S38326
Contains Protein kinases signatures and profile
AA70-102;Protein kinases signatures and profile AA196-208"
/ codon_start=1
/ product="serine/threonine-specific protein kinase-like"
/ protein_id="CAB75903.1"
/ db_xref="GI:7076788"
/ translation="MAFKKRNEICKNLLPSSSGLDDHLSSCKSSSSSATAHKTEGEIL
SSTTVKSFNFELKLATRNFRSDSVVGEFGFCVFRGWLDETTLTPKSSSGLVIAVK
RLNPDGFGQHREWLTEINYLGLSHPNLVKLIGYCLEDEQRLLVYEFMHKGSLENHLF
ANGNKDFKPLSWILRIKVALDAAKGLAFLHSDPVKVIYRDIKASNILLSDFNAKLSD
FGLARDGPMGEQSYVSTRVMGTFGYAAPEYVSTGHLNARSDVYSFGVVLELLCGRQA
LDHNRPAKEQNLVDWARPYLTSRRKVLIVDTRLNSQYKPEGAVRLASIAVQCLSFEP
KSRPTMDQVVRALVQLQDSVVKPANVDPLKVKDTKKLVGLKTEDKYQRNGLNKKTVGL
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exon 40736..40780
/ gene="T22E16.110"
/ number=1
intron 40781..40867
/ gene="T22E16.110"
/ number=1
exon 40868..41170
/ gene="T22E16.110"
/ number=2
intron 41171..41262
/ gene="T22E16.110"
/ number=2
exon 41263..41398
/ gene="T22E16.110"
/ number=3
intron 41399..41476
/ gene="T22E16.110"
/ number=3
exon 41477..41622
/ gene="T22E16.110"
/ number=4
intron 41623..41701
/ gene="T22E16.110"
/ number=4
exon 41702..41825
/ gene="T22E16.110"
/ number=5
intron 41826..42012

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/ gene="T22E16.110"
/ number=5
exon      42013..42437
/ gene="T22E16.110"
/ number=6
gene      43498..46111
/ gene="T22E16.120"
CDS       join(43498..43673,43774..43851,44952..45122,45264..45295,
45343..45432,45478..45556,45639..45788,45874..45961,
46046..46111)
/ gene="T22E16.120"
/ note="similarity to Serine/arginine-rich protein/putative
splicing factor, Arabidopdis thaliana, EMBL:AF099940
Contains Prenyl group binding site (CAAX box)
AA306-309;Eukaryotic putative RNA-binding region RNP-1
signature AA88-95"
/ codon_start=1
/ product="putative RNA binding protein"
/ protein_id="CAB75904.1"
/ db_xref="GI:7076789"
/ translation="MRRYSPPYSPRRRGYGGGRSPPPPPRRGYGGGGGGGRRGS
SHGSLLVRNIPLCDRPEELREPFERFGPVRDVYIPRDYYSQGPRGFAFVEFVDAYDAG
EAQRSMNRRSFAGREITVVVASESRKRPEEMRVKTRTRSREPSGSRDRSHAKFTQILA
QLDWDALVYTQLEKALVYTCSHGSRSRSRISRSRSPRRPDSRSRYSRYSYPAPRRR
GGPPRGEEDENYSRRSYSPGYEGAAAAAPDRDRNGDNEIREKPGYEAEDRRRGGRAVS
RSPSGSRSRSECVSVSLKTPYSGLSKIFCLVM"
exon      43498..43673
/ gene="T22E16.120"
/ number=1
intron    43674..43773
/ gene="T22E16.120"
/ number=1
exon      43774..43851
/ gene="T22E16.120"
/ number=2
intron    43852..44951
/ gene="T22E16.120"
/ number=2
exon      44952..45122
/ gene="T22E16.120"
/ number=3
intron    45123..45263
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exon      45264..45295
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intron    45296..45342
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/ number=4
exon      45343..45432
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/ number=5
intron    45433..45477
/ gene="T22E16.120"
/ number=5
exon      45478..45556
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/ number=6
intron    45557..45638
/ gene="T22E16.120"
/ number=6
exon      45639..45788
/ gene="T22E16.120"
/ number=7
intron    45789..45873
/ gene="T22E16.120"
/ number=7
exon      45874..45961
/ gene="T22E16.120"
/ number=8
intron    45962..46045
/ gene="T22E16.120"
/ number=8
exon      46046..46111

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/gene="T22E16.120"
/number=9
gene 46831..48567
/ gene="T22E16.130"
CDS join(46831..46897,46996..47061,48030..48171,48275..48410,
48508..48567)
/ gene="T22E16.130"
/ note="strong similarity to FIERG2 protein, Oryza sativa,
PIR:T04363"
/ codon_start=1
/ product="elicitor responsive/phloem-like protein"
/ protein_id="CAB75905.1"
/ db_xref="GI:7076790"
/ translation="MAVGILEVSLISGKGLKRSDFLGKIDPYVEIQKGQTRKSSVAK
EDGGRNPTWNDKLKWRAEFPGSGADYKLIVKMDHDTFSSDDFIGEATVHVKELLEMG
VEKGTAELRP TKYNIVSDLSFVGELLIGVSYSLLQDRGMDGEQFGCWKHSQVD"
exon 46831..46897
/ gene="T22E16.130"
/ number=1
intron 46898..46995
/ gene="T22E16.130"
/ number=1
exon 46996..47061
/ gene="T22E16.130"
/ number=2
intron 47062..48029
/ gene="T22E16.130"
/ number=2
exon 48030..48171
/ gene="T22E16.130"
/ number=3
intron 48172..48274
/ gene="T22E16.130"
/ number=3
exon 48275..48410
/ gene="T22E16.130"
/ number=4
intron 48411..48507
/ gene="T22E16.130"
/ number=4
exon 48508..48567
/ gene="T22E16.130"
/ number=5
gene 48847..53607
/ gene="T22E16.140"
gene complement(join(48847..49264,49345..49608,49799..50742,
51076..51276,51434..51543,51625..51751,51953..52126,
52233..52862,52946..53195,53268..53344,53431..53607))
/ gene="T22E16.140"
CDS complement(join(48847..49264,49345..49608,49799..50742,
51076..51276,51434..51543,51625..51751,51953..52126,
52233..52862,52946..53195,53268..53344,53431..53607))
/ gene="T22E16.140"
/ note="similarity to AP-3 complex beta3A subunit, Homo
sapiens, EMBL:HSU91931"
/ codon_start=1
/ product="adaptor protein/ adaptin-like"
/ protein_id="CAB75906.1"
/ db_xref="GI:7076791"
/ translation="KLQLGLLRIGTDAHLYDDPEDVNIAPLLDSKFESKCEALKRLL
ALIAQGFVDVSNFFPQVVKNVASQSSEVKKLVLYLLQYAEKRPNEALLSINYFQKDLG
DNPPLVRAWALRTMAGIRLHVIAPLALAAVSKCARDPAVYVRRCAANALPKLHDLRLE
EHASAIEELVGILLNDHSPGVVGAAAAAFTSICPNNFKLIGKNYKKLCQILPDVEEWG
QILLIGTLLRVVVARHGLVRESLMLSIHGTNSNGFCEKDGLGRDRLTDKEDGGKSDSF
DVNLVSLVSKCYIQGPDEYLSRSSCTDTVSSAFDTKETTSIAHNEDVKILLQCTSPLL
WSNNSAVVLAAGVQWIMAPLEDVKKIVKPLFLLRSSASKYVVLNCNIVFAKAVPS
LFAPHFENFFICSSDAYQVKAYKLEMLSLIATTSSIASILREFEDIKDPDRRFAADT
VAAIGLCAKRLMTIPTTCLDGLLALVRQESFAGDFESADGEAGVLVQAVMSIQTMIER
DPLRHEKVLILQFRSLDSIKVAAARATIIMVGVYCSLGHII PRMLTTITKYLAWSFK
SEASETKLQILNTIAKVLI SAEAGDFHMLKRIVVYVFELGEYDLSYDIRDRTRFLKKL
LSCKLASHEPAEDSVASQENIAAHVVEHVFGKRLKSVSPITLHNRFYLPGLSLSQIVLH
AAPGYEPLPKPCS FVYEEQDQLSDLDKQREAAADLDGSEESSETGDENGSSDYDSESS
NGSDFSSSEGDERTVSNANDANDPAAPLIQISETSVSADQEELRSRRALDLWLDQDPSTSN
QTPSALNSNQSSYAKISIGDVGSRVKPKSYSLVDPNGSGSLKVDYAFLEVSNNVSP LH
VCVEVLFFENSSAEPILEVNLEDEESMKVADSSEQTLVGKANASYNNIPTLIPMEEISC

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LEPHQSTKRLLQVRFHHLLPMRLTLHYNEKKVPVKLRPDLGYLVKPFMSIEEFLAT
ESRLPGMFEYSRRKIMFTSLTDFLTWVVLFTFGRCTFDDHVKDSRTENGDKFLSICE
SITLKVLSNSNLHLVSDLPVANSLEDATGLRLRFSSKILSSEIPLLITITVEGKCTE
VLNLTVKINCETVFGNLNLRNRIANFMVEPSSSAT"
exon      complement (48847..49264)
          /gene="T22E16.140"
          /number=1
intron    complement (49265..49344)
          /gene="T22E16.140"
          /number=1
exon      complement (49345..49608)
          /gene="T22E16.140"
          /number=2
intron    complement (49609..49798)
          /gene="T22E16.140"
          /number=2
exon      complement (49799..50742)
          /gene="T22E16.140"
          /number=3
intron    complement (50743..51075)
          /gene="T22E16.140"
          /number=3
exon      complement (51076..51276)
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          /number=4
intron    complement (51277..51433)
          /gene="T22E16.140"
          /number=4
exon      complement (51434..51543)
          /gene="T22E16.140"
          /number=5
intron    complement (51544..51624)
          /gene="T22E16.140"
          /number=5
exon      complement (51625..51751)
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          /number=6
intron    complement (51752..51952)
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          /number=6
exon      complement (51953..52126)
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intron    complement (52127..52232)
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exon      complement (52233..52862)
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intron    complement (52863..52945)
          /gene="T22E16.140"
          /number=8
exon      complement (52946..53195)
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          /number=9
intron    complement (53196..53267)
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          /number=9
exon      complement (53268..53344)
          /gene="T22E16.140"
          /number=10
intron    complement (53345..53430)
          /gene="T22E16.140"
          /number=10
exon      complement (53431..53607)
          /gene="T22E16.140"
          /number=11
gene      54647..55891
          /gene="T22E16.150"
gene      complement (join (54647..54756,54867..55006,55261..55353,
55505..55605,55669..55764,55847..55891))
          /gene="T22E16.150"
CDS       complement (join (54647..54756,54867..55006,55261..55353,
55505..55605,55669..55764,55847..55891))
          /gene="T22E16.150"

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/note="similarity to hypothetical protein,
Schizosaccharomyces pombe, EMBL:AL133156"
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/product="putative protein"
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/db_xref="GI:7076792"
/translation="MAKYFDIDDILIEEEFVPLFHKGTANGVTIDPSAETNCVSILLP
SAKAEQGSKVELPFWLAHELHLRQAVTINLPPCFDQKTRLEVQADAAAYVDLRSRCPYF
YEFGCKIEPLVTDRTLGIILLSTAFKIRYKEALTKVYTAAHITASKYLSFLTKEETNLY
EAAHLSMTAFKKWRTGQPRFQRASILGRKRKDSN"
exon      complement(54647..54756)
          /gene="T22E16.150"
          /number=1
intron    complement(54757..54866)
          /gene="T22E16.150"
          /number=1
exon      complement(54867..55006)
          /gene="T22E16.150"
          /number=2
intron    complement(55007..55260)
          /gene="T22E16.150"
          /number=2
exon      complement(55261..55353)
          /gene="T22E16.150"
          /number=3
intron    complement(55354..55504)
          /gene="T22E16.150"
          /number=3
exon      complement(55505..55605)
          /gene="T22E16.150"
          /number=4
intron    complement(55606..55668)
          /gene="T22E16.150"
          /number=4
exon      complement(55669..55764)
          /gene="T22E16.150"
          /number=5
intron    complement(55765..55846)
          /gene="T22E16.150"
          /number=5
exon      complement(55847..55891)
          /gene="T22E16.150"
          /number=6
gene      57549..58578
          /gene="T22E16.160"
gene      complement(join(57549..57858,57976..58294,58425..58578))
          /gene="T22E16.160"
CDS       complement(join(57549..57858,57976..58294,58425..58578))
          /gene="T22E16.160"
          /note="strong similarity to expansin At-EXP6, Arabidopsis
thaliana, EMBL:AT30480
Contains Prokaryotic membrane lipoprotein lipid attachment
site AA73-83"
          /codon_start=1
          /product="expansin-like protein"
          /protein_id="CAB75908.1"
          /db_xref="GI:7076793"
          /translation="MAINPLILLTIFPLFLLLSFTDAGIPRVFSGGSWQTAHATFYGG
NDASGTMGGACGYGNLYSQGYGTNTAALSTSLFNSGQSCGACFEIKCVNDPKWCHPGN
PSVFVTATNFCPPNLAQPSDNGGCNPPRSHFDLAMPVFLKIAEYRAGIVPISYRRVA
CRKSGGIRFTINGHRYFNLVLITNVAGAGDIARTSVKGSKTGWMSLTRNWGQNWQNSNA
VLVGQSLSFRTSSDRRTSTSWNIAPSNWQFGQTFVGKNFRV"
exon      complement(57549..57858)
          /gene="T22E16.160"
          /number=1
intron    complement(57859..57975)
          /gene="T22E16.160"
          /number=1
exon      complement(57976..58294)
          /gene="T22E16.160"
          /number=2
intron    complement(58295..58424)
          /gene="T22E16.160"
          /number=2
exon      complement(58425..58578)

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/gene="T22E16.160"
/number=3
gene      61708..64600
          /gene="T22E16.170"
CDS       join(61708..61816,61982..62045,62264..62372,62473..62997,
          63276..63575,63661..63984,64090..64296,64418..64600)
          /gene="T22E16.170"
          /note="similarity to various predicted proteins"
          /codon_start=1
          /product="putative protein"
          /protein_id="CAB75909.1"
          /db_xref="GI:7076794"
          /translation="MGKLGKKARKFAKKNLQSVKRSRKLKPFIKKKFAKRNERHQAG
          DKQEKKVEQQPKKRCQEEEFQDIAIDAVFGKDDDEVLRDGDSDSDGYLDEQSNITIN
          HPMQLVNETSDIMCKVKLSRSFLATCCDMVDKEQYVPALVRLLNWYRAACQYGHEPS
          GIARPNIIYYDIEDSETFAKVII FVLQKADHTFRSILGLSDSSTKEKILKLNPKWDS
          LKPLVKSFFRSTLHLVKQAGDLEIISFTLTQLRVSI VFLAAFDDLLKKLIKISVHLWV
          TGEETISQQAFLILKDISMVFNSCFDSCLINMYKAFLHDCDIPKANSEQRPFRLRDSL
          VELCSQDVQKSYTKASVSITQLAKLLKMALATKNKEAVEKIHSGEYINCVDLWVNFIS
          ANVQDCDLQPLLYTIVQVINGVAQLIIGPRYLLLRVKCIHWNHLSRTSGIFIPIASL
          VLDMLEYKTTNDGEKQEQKLEAVSTVKLPKNWLKSNFQEQCIFSVIELLAVHFAQWS
          FHSIFPDLATIPVMRLKKFHERSTMEGLKRVVKRFIEQVESNIEFVQRKRDDVTFSPN
          DQQSADTFMQLEKQANAPYTYQYQSIIDKALGTNKKKKK"
exon      61708..61816
          /gene="T22E16.170"
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intron    61817..61981
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          /number=1
exon      61982..62045
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          /number=2
intron    62046..62263
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          /number=7
exon      64418..64600
          /gene="T22E16.170"
          /number=8
gene      76653..77604
          /gene="T22E16.180"
CDS       join(76653..76761,76878..77011,77097..77176,77268..77360,
          77448..77604)
          /gene="T22E16.180"
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          IMMUNOPHILIN), rabbit, SWISSPROT:FKB4_RABIT"

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101041 aagggttaaac cgcagagatt ggtgaaggat gtttgattgg ccctaactgt gctataggcc
101101 ctggctgtgt tgttgagtcc ggggttagac tatcgactg cacggtaatg cgtgggttac
101161 acgtgaagag atatcggtgt atctcgagta gtatcattgg gtggcactcg acggctcgac
101221 aatgggctcg ggtcgagaac atgtccatac ttgggaaaaa tgtttacgtg tgcgatgaga
101281 tatctttaa tggagggtt gtgtgcata acaaagagat caaatcagac atcttgaaac
101341 cagatatagt gatgtgatga caatttgggt gatttgcctg tatttttcat tttttgtgc
101401 gaatacgatt tctaatttaa agtcatgaaa aagtaaaatt ttcaatgttt tataagagtc
101461 tagctcctag taagcctttc gacaagtttc ctaagaatat caaagacgct cttgagattg
101521 aagggttaaac tagtgatgtg tgaatcttga catatgatgc tgggaatata tgttgttga
101581 agttagatct aattaattta tgtgtgtctc ttgagttaa agatgtttga tctaagtga
101641 atcatgagaa gaggtcgtga tcttgttctt cctttttgta cgtgccatgg ccttggctcg
101701 gattctgaat ttttcttagg tacattgctg acaattgaag gtcaggatgt agcaaatcaa
101761 tgtattcatgc ggttgggtt acttaagaag taaaagagat atcagtctca gcgagcagat
101821 aaaacttttg ttcaaatga tccacagagc agacgtacga tttaatcttt caattaatca
101881 tacaataact aggaatgag aatcattag cagagattat aaaacctagg gcattgatgg
101941 gaaagggatt aaaacagcaa aactataaac agagttaaag agaacaaaaa ccaaagtctt
102001 ttggacagaa gagattataa aagtgaaaac cacacgcctt agcatagcct tcccccggt
102061 aagctcccaa gcagtgagg gagccctggg cacccttctc cacaatatgg acaaggagta
102121 tcgtcgccct cgtcatcttc ttcgatctg aaagtctctt gtttgacacg agatattagg
102181 ctacgtaatt ggatccaata ggctttccca aaaccataca gtgtttacat acggaatttg
102241 cggcgcttct tgtgaccagt cattagccac aactaagata acattgtaac tcataaacat
102301 ccaacaaact aagatgttct tcgaacttgg tctctcttgg gatgcttttg gcgattacca
102361 tcagatttgt agatgtataa tggggagcag gattttccac tgacaaaaat gcaatttcca
102421 ctaacatctt gtttagtctc tcactcttac cccctaaaaa aatgtatata tcagttatca
102481 actaacatgt aaaattgcac tgcacataca tatatatata tatatatata tatataatat
102541 gtaataaaaa agaactaggg tttaagtaaa ggacaatcac ttttgggttc gaagtcgatt
102601 acatcatcca gactgtcagg tttctctca ccataagcag tgattgacac ctcaccatga
102661 taacctacaa atcacagaga tcgagatctc tgggcatggt ggtttcgacg gagatcgaga
102721 aaacagaaaa ttgattttag aagtgaagg cctatcaatg ttttacattt aagcacagta
102781 aacattttaa gccagccta gcccattaa aggtaaatct aatttgctac gaattcgggt
102841 gttaattatt aaaccatcgg ttttagttcat caaacgcaa ccaaagcaa taaccgaata
102901 atttctcgag aaaaaataat gactttccgg tgaagatttt tttttacgac ggcttctcct
102961 gacaacggaa ggtgttgaga aagtggcgga atttgatttt gtttctctc ctctcctatc
103021 taaacaaggt ctgtttctgt gagatccaga tattcaattt ggattcaaaa tcgtgaattg
103081 ggttttggat tgatttctgt tactggctg tgtgcttga tctgaatgtt gtttcatctc
103141 ctagtgtgca gatttactga tgatgggaat aagcaaaacg gagatcaatt tgcggagatt
103201 gctttccgct gcacctaacc agcaaatca gtcgaagctt

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IDENTIFIERS

dbEST Id: 4171593
 EST name: AV442303
 GenBank Acc: AV442303
 GenBank gi: 7612710

CLONE INFO

Clone Id: APZ05f10_r (5')
 DNA type: cDNA

PRIMERS

PolyA Tail: Unknown

SEQUENCE

CTCGTTTGCTCCGCTTAAGCACCATGAAGGTCACCGTCGTCTCCCGCAGCGGCAGAGAAG
 TCCTCAAAGCTCCCCCTTGACCTCCCCGATTCGGCGACTGTTGCTGATCTGCAAGAAGCGT
 TTCATAAGAGAGCTAAGAAGTTTACCCGTCGAGGCAAAGACTGACTCTTCCCGTGACTC
 CTGGATCGAAGGACAAACCTGTTGTCCTCAATAGCAAGAAATCACTGAAGGAGTACTGTG
 ATGGAAACAACAACCTCCTTAAGTGTAGTCTTCAAAGACCTGGGGGCACAAGTTTCCTACC
 GCACACTCTTCTTCTTCGAGTATCTTGGCCCTCTCCTTATCTACCCTGTCTTTTACTACT
 TCCCTGTTTACAAGTTTCTTGGTTATGGAGAGGACTGTGTGATCCATCCGGTCCAGACGT
 ACGCTATGTACTACTGGTGCTTTCACTACTTCAAACGGATCTTAGAAACGTTTTTCGTAC
 ATCGGTTACGCCACGCAACCTCCCCAATCGGGAATGTGTTTCAGGAAGTGTGCTTATTACT
 GGAGCTTTGGTGTC

Entry Created: Apr 19 2000
 Last Updated: Nov 14 2000

LIBRARY

dbEST lib id: 4063
 Lib Name: Arabidopsis thaliana above-ground organ two to six-week old
 Organism: Arabidopsis thaliana
 Strain: Columbia
 Tissue type: aboveground organs
 Develop. stage: two to six-week old
 Vector: pBluescriptII SK-
 R. Site 1: EcoRI
 R. Site 2: XhoI

SUBMITTER

Name: Erika Asamizu
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 Address: Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
 E-mail: asamizu@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>

CITATIONS

Medline UID: 20363093
 Title: A large scale analysis of cDNA in Arabidopsis thaliana:
 Generation of 12,028 non-redundant expressed sequence tags
 from normalized and size-selected cDNA libraries
 Authors: Asamizu, E., Nakamura, Y., Sato, S., Tabata, S.
 Citation: DNA Res. 7: 175-180 2000

MAP DATA

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IDENTIFIERS

dbEST Id: 3548916
 EST name: sf37a01.y1
 GenBank Acc: AW203676
 GenBank gi: 6502303

CLONE INFO

Clone Id: GENOME SYSTEMS CLONE ID: Gm-c1028-2113 (5')
 Source: ResGen, Invitrogen Corp.
 Insert length: 1005
 DNA type: cDNA

PRIMERS

PolyA Tail: Unknown

SEQUENCE

ACGAGGGTGATTAAAGTCTGTGTTGTTTCAGCTTCATTTTCCCCCGCCACCTTCTCTGGTG
 GTTTGGGGTTGACTGTGACAAGCTTCCTGATACTGGCTAATGCTTCTTGTGAGAAATT
 AGAGGGAAGCATTTGAACTATTCAAAGTTTTGGAATGCTAATCCCTCTGCAGAAAAGCAG
 GTCAAGTTGTCTAGCAAAGCTGGCATGCTTTTGCTGTACACTCCTGCTTTTCTTGCTGGC
 CTTGCATCCTTCTGGGTCTTCTCATCAAGGGCTCAGATTCACCATCCTTCAATCTGCT
 GTTACTCTGCACTACTTCAAGAGGGTCTTTGAGGTCTGTTTATTACAAATATAGTGGA
 GGCATGACACTTGAATCTGCAATCCCCATCACTCTGAGTTATTTCTCTCAGCTGTAAT
 ATGGTCTATTCTCAACACCTAACAAAAGGGTNTCCAGAACCACCAATCAATCTGTTCTAC
 CCTGGCATTGTGTTGTTTCTAGTTGGCATCATTGGCAACTTCTACCACCATTACCTTCTG
 TCCAAATTGAGGGGAAAGGGTGAAAAGGAGTACAAGATTCCAAAG

Quality: High quality sequence stops at base: 415

Entry Created: Dec 1 1999

Last Updated: Dec 2 2001

COMMENTS

This clone is available through: ResGen, Invitrogen Corp.
 2130 South Memorial Parkway Huntsville, AL 35801 For further
 information call: (800)-533-4363 or contact via email:
 ccu@resgen.com

PUTATIVE ID Assigned by submitter
 WP:C15F1.C CE20509 ;

LIBRARY

dbEST lib id: 2720
 Lib Name: Gm-c1028
 Organism: Glycine max
 Tissue type: roots of 'Supernod' plants
 Lab host: DH10B
 Vector: pBluescript II XR
 R. Site 1: EcoRI
 R. Site 2: XhoI
 Description: The mRNA was isolated from roots of Glycine max 'Supernod'
 plants generously donated by Dr. Gary Stacey. The seedlings
 were inoculated with Bradyrhizobium japonicus, strain
 USDA110 priot to harvest. Stratagene's cDNA synthesis Kit
 (catalog number 200401) was used to synthesize the cDNA.
 First-strand synthesis was performed with 5-methyl dCTP,
 hence the ligated cDNA was hemimethylated. A modification of
 Stratagene's first-strand synthesis primer was used. An
 'anchor' nucleotide (V=A,C, or G) was added to the 3' end of
 the primer [GAGAGAGAGAGAGAGAGAGAACTAGTCTCGAG(T)18V] to
 anchor the primer at the 5' end of the poly(A) tract. After
 second-strand synthesis, the cDNA ends were filled in with
 cloned Pfu DNA polymerase, ligated to EcoRI adapters and
 subsequently phosphorylated. The XhoI site within the
 first-strand synthesis primer was then restricted by
 digestion with XhoI; all XhoI sites in the cDNA would be
 protected by their hemimethylated status. The cDNA
 constructs were size-fractionated with a 500bp cutoff, using
 GibcoBRL Life Technologies' cDNA Size Fractionation column.
 The column eluent was then ligated into Stratagene's
 pBluescript II XR Predigested vector (pBluescript II SK(+)
 that has been digested with EcoRI and XhoI, and
 phosphorylated by Stratagene). Both the white and blue
 colonies appear to contain recombinant plasmids with cDNA
 inserts, based on size (n=25). This library was constructed

by Dr. Paul Keim and Dr. Virginia Coryell.

SUBMITTER

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Fax: 314 286 1810
E-mail: est@watson.wustl.edu

CITATIONS

Title: Public Soybean EST Project
Authors: Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin
,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising
,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M.,
Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T.,
Jackson,Y., Cardenas,M., McCann,R., Waterston,R., Wilson,R.
Year: 1999
Status: Unpublished

MAP DATA

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IDENTIFIERS

dbEST Id: 3592347
 EST name: sf18d10.y1
 GenBank Acc: AW234714
 GenBank gi: 6567087

CLONE INFO

Clone Id: GENOME SYSTEMS CLONE ID: Gm-c1028-332 (5')
 Source: Genome Systems, Inc.
 Insert length: 690
 DNA type: cDNA

PRIMERS

PolyA Tail: Unknown

SEQUENCE

TCCTCATCAAGGGCTCAGATTCACCATCCTTCAATCTGCTGTACTCTGCACTACTTCAA
 GAGGGTCTTTGAGGTCTGTATTATTCACAAATATAGTGGAGGCATGACACTGAATCTGC
 AATCCCCATCACTCTGAGTTATTTCTCTCAGCTGTAACATATGGTCTATTCTCAACACCT
 AACAAAAGGGTTTCCAGAACCACCAATCAATCTGTTCTACCCTGGCATTGTGTTGTTCT
 AGTTGGCATCATTGGCAACTTCTACCACCATTACCTTCTGTCCAAATTGAGGGGAAAGGG
 TGAAAAGGAGTACAAGATTCCAAAGGGTGGCTTTTGTGAGCTTGTGATTTGCCCCCACTA
 CTTCTTTGAGATTACTGTGTTTTATGGGATCTTCTTCATTTCTCAGACATTATATTCATT
 CGCTCTCGCTGTAGGCACTACTATGTACTTGGTGGGTAGGAGTTACTCAACTAGGAAATG
 GTATCTTTCTAAGTTTGAAGATTTCCCTAAGCATGTTAAGGCTGTCATCCCATTGTCTT
 C

Quality: High quality sequence stops at base: 414

Entry Created: Dec 13 1999

Last Updated: Jul 17 2000

COMMENTS

This clone is available through: Genome Systems, Inc. 4633
 World Parkway Circle St. Louis, Missouri 63134 For further
 information call: (800) 430-0030 or (314) 427-3222 FAX:(888)
 919-3324 or (314) 427-3324 or contact:
 clones@genomesystems.com or info@genomesystems.com web site:
 www.genomesystems.com

PUTATIVE ID

Assigned by submitter
 SW:S5A2_MACFA Q28892 3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 2
 ;

LIBRARY

dbEST lib id: 2720
 Lib Name: Gm-c1028
 Organism: Glycine max
 Tissue type: roots of 'Supernod' plants
 Lab host: DH10B
 Vector: pBluescript II XR
 R. Site 1: EcoRI
 R. Site 2: XhoI

Description: The mRNA was isolated from roots of Glycine max 'Supernod'
 plants generously donated by Dr. Gary Stacey. The seedlings
 were innoculated with Bradyrhizobium japonicus, strain
 USDA110 prior to harvest. Stratagene's cDNA synthesis Kit
 (catalog number 200401) was used to synthesize the cDNA.
 First-strand synthesis was performed with 5-methyl dCTP,
 hence the ligated cDNA was hemimethylated. A modification of
 Stratagene's first-strand synthesis primer was used. An
 'anchor' nucleotide (V=A,C, or G) was added to the 3' end of
 the primer [GAGAGAGAGAGAGAGAGAACTAGTCTCGAG(T)18V] to
 anchor the primer at the 5' end of the poly(A) tract. After
 second-strand synthesis, the cDNA ends were filled in with
 cloned Pfu DNA polymerase, ligated to EcoRI adapters and
 subsequently phosphorylated. The XhoI site within the
 first-strand synthesis primer was then restricted by
 digestion with XhoI; all XhoI sites in the cDNA would be
 protected by their hemimethylated status. The cDNA
 constructs were size-fractionated with a 500bp cutoff, using
 GibcoBRL Life Technologies' cDNA Size Fractionation column.
 The column eluent was then ligated into Stratagene's
 pBluescript II XR Predigested vector (pBluescript II SK(+)
 that has been digested with EcoRI and XhoI, and

phosphorylated by Stratagene). Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=25). This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell.

SUBMITTER

Name: Shoemaker R/Public Soybean EST Project
Lab: Public Soybean EST Project
Institution: Washington University School of Medicine
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Fax: 314 286 1810
E-mail: est@watson.wustl.edu

CITATIONS

Title: Public Soybean EST Project
Authors: Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin
,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising
,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M.,
Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T.,
Jackson,Y., Cardenas,M., McCann,R., Waterston,R., Wilson,R.
Year: 1999
Status: Unpublished

MAP DATA

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IDENTIFIERS

dbEST Id: 3799016
 EST name: sf37a01.x1
 GenBank Acc: AW396663
 GenBank gi: 6915202

CLONE INFO

Clone Id: GENOME SYSTEMS CLONE ID: Gm-c1028-2113 (3')
 Source: ResGen, Invitrogen Corp.
 Other ESTs on clone: sf37a01.y1
 Insert length: 1005
 DNA type: cDNA

PRIMERS

PolyA Tail: Unknown

SEQUENCE

TTTTTTTTTCAACCAAGTTAAAAAATAGTTTATTAAATCACTCAAACCTGGATGTTGGA
 GAGCTGCAATTCCAATAAACACAATCTAGCAGCACACTTACAACCTCAAGTAGAATTAGAT
 GTTCATTACAACATTTAGAAGACAAATGGGATGACAGCCTTAACATGCTTAGGGAAATCT
 TCAAACCTAGAAAGATACCATTTCCTAGTTGAGTAACTCCTACCCACCAAGTACATAGTA
 GTGCCCTACAGCGAAAGCGAATGAATATAATGTCTGAGAAATGAAGAAGATCCCATAAAAAC
 ACAGTAATCTCAAAGAAGTAGTGGGGGCAAAATCACAAGCTCAAAAAAGCCACCCTTTGGA
 ATCTTGTACTCCTTTTACCCTTTCCCTCAATTTGGACAGAAGGTAATGGTGGTAGAAG
 TTGCCAATGATGCCAACTAGAAACAACACAGTGCCAGGGTAGAA

Quality: High quality sequence stops at base: 425

Entry Created: Feb 7 2000

Last Updated: Dec 2 2001

COMMENTS

This clone is available through: ResGen, Invitrogen Corp.
 2130 South Memorial Parkway Huntsville, AL 35801 For further
 information call: (800)-533-4363 or contact via email:
 ccu@resgen.com

PUTATIVE ID

Assigned by submitter
 SW:S5A1_HUMAN P18405 3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1
 ;

LIBRARY

dbEST lib id: 2720
 Lib Name: Gm-c1028
 Organism: Glycine max
 Tissue type: roots of 'Supernod' plants
 Lab host: DH10B
 Vector: pBluescript II XR
 R. Site 1: EcoRI
 R. Site 2: XhoI
 Description: The mRNA was isolated from roots of Glycine max 'Supernod' plants generously donated by Dr. Gary Stacey. The seedlings were innoculated with Bradyrhizobium japonicus, strain USDA110 priot to harvest. Stratagene's cDNA synthesis Kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V=A,C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAGAGAGAACTAGTCTCGAG(T)18V] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA polymerase, ligated to EcoRI adapters and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GibcoBRL Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+)) that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene. Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=25). This library was constructed

by Dr. Paul Keim and Dr. Virginia Coryell.

SUBMITTER

Name: Shoemaker R/Public Soybean EST Project
Lab: Public Soybean EST Project
Institution: Washington University School of Medicine
Address: 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
E-mail: est@watson.wustl.edu

CITATIONS

Title: Public Soybean EST Project
Authors: Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin
,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising
,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M.,
Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T.,
Jackson,Y., Cardenas,M., McCann,R., Waterston,R., Wilson,R.
Year: 1999
Status: Unpublished

MAP DATA

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IDENTIFIERS

dbEST Id: 3925593
 EST name: 660060A06.y1
 GenBank Acc: AW506800
 GenBank gi: 7145319

CLONE INFO

Plate: 660060 Row: A Column: 06
 DNA type: cDNA

PRIMERS

PolyA Tail: Unknown

SEQUENCE

GGAATTGGGCACGAGCAAGTACTTTCGGGTACGAGGGGGAGCGGGCCATGCACCCTGTCCA
 GACCTACGCCATGTACTACTGGTGCTTCCACTACTTCAAGCGGGTCATGGAGACGTTCTT
 CGTGCACCGCTTCAGCCACGCGACGTCGCGCTCTCGAACGCTTTCAGGAAGTGTGCCTA
 CTACTGGACCTTCGGCGCTTACATTGCTTACTACTGCAACCACCGCTGTACACCCAGT
 GAGTGATCTGCAGATGAAGATTGGGTTTGGTTTGGGGTCGCTGCCAGGTCGCGAACTT
 CTACTGCCACATCCTGTGCGGAACCTCAGGAGCCCAAGCGGCAGCGCGGGTACCAGAT
 CCCCCGCGTTTCTTGTTCACATCGTGACCTGCGCCAATTACACCACCGAGATCTATCA
 GTGGGTGCGGCTTCAACATCGCCACGACCGTGGCAGGTTACGTCCTTGTCTGCGGC
 GGCAGGCATCATGACCAACTGGGCGCTCGGCAAGCACAGCCGCTCTGAAGAAGCTGTTTGA
 CGGCAAGGATGGGAGGCCCAAGTACCCTCGCCGGT

Entry Created: Mar 3 2000

Last Updated: Mar 3 2000

LIBRARY

dbEST lib id: 2329
 Lib Name: 660 - Mixed stages of anther and pollen
 Organism: Zea mays
 Cultivar: Ohio43
 Organ: anthers
 Tissue type: whole premieotic anthers to pollen shed
 Develop. stage: premieotic anthers to pollen shed
 Lab host: XLRLR
 Vector: Lambda Zap
 R. Site 1: EcoRI
 R. Site 2: XhoI
 Description: Anther and pollen cDNA library. Directionally sequenced with
 5' end at the EcoRI site. Created by Amie Franklin.

SUBMITTER

Name: Walbot V
 Lab: Department of Biological Sciences
 Institution: Stanford University
 Address: 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 E-mail: walbot@stanford.edu

CITATIONS

Title: Maize ESTs from various cDNA libraries sequenced at Stanford
 University.
 Authors: Walbot, V.
 Year: 1999
 Status: Unpublished

MAP DATA

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IDENTIFIERS

dbEST Id: 4003115
 EST name: sj64d10.y1
 GenBank Acc: AW570599
 GenBank gi: 7235270

CLONE INFO

Clone Id: GENOME SYSTEMS CLONE ID: Gm-c1033-2060 (5')
 Source: ResGen, Invitrogen Corp.
 DNA type: cDNA

PRIMERS

PolyA Tail: Unknown

SEQUENCE

GCACGAGCTTAACACAAGGGCTTCCAGAACCACCAATCGATCTGTTGTATCCTGGCATTG
 TTTTGTGTGTGGTGGGCATCATTGGCAACTTCTACCACCACTACCTTCTATCCAACCTAA
 GGGGAAAGGGTGAAAAGGAGTACAAGATTCCAAAGGGTGGCATGTTTGAGCTTGTCATAT
 GTCCCCACTACCTGTTTGAGATTATTGAGTTTATGGGTTCTCCTTCATTTCGCAGACGC
 TATATGCATTCTCTTTCACCGTAGGCACTACTTTATACTTGCTAGGTAGGAGTTATTCAA
 CTAGGAA

Entry Created: Mar 13 2000
 Last Updated: Dec 3 2001

COMMENTS

This clone is available through: ResGen, Invitrogen Corp.
 2130 South Memorial Parkway Huntsville, AL 35801 For further
 information call: (800)-533-4363 or contact via email:
 ccu@resgen.com

PUTATIVE ID

Assigned by submitter
 SW:S5A1_RAT P24008 3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 ;

LIBRARY

dbEST lib id: 3799
 Lib Name: Gm-c1033
 Organism: Glycine max
 Tissue type: 'Desloy 5710' seedling roots
 Lab host: DH10B
 Vector: pBluescript II XR
 R. Site 1: EcoRI
 R. Site 2: XhoI

Description: This cDNA library was constructed from mRNA isolated from
 'Desloy 5710' seedling roots. Tissue was taken from
 7-day-old seedlings that had been propagated on paper towels
 with distilled water. Tissue was taken from the tip to the
 first lateral root, usually about 3cm from the tip, and
 flash-frozen in liquid nitrogen. Stratagene's cDNA Synthesis
 Kit (catalog number 200401) was used to synthesize the cDNA.
 First-strand synthesis was performed with 5-methyl dCTP,
 hence the ligated cDNA was hemimethylated. A modification of
 Stratagene's first-strand synthesis primer was used. An
 'anchor' nucleotide (V=A, C, or G) was added to the 3' end
 of the primer [GAGAGAGAGAGAGAGAGAGAACTAGTCTCGAG(T)18V] to
 anchor the primer at the 5' end of the poly(A) tract. After
 second strand synthesis, the cDNA ends were filled in with
 cloned Pfu DNA, ligated to EcoRI adapters and subsequently
 phosphorylated. The cDNA was then precipitated and
 redissolved in sterile, RNase-, DNase-free water. The XhoI
 site within the first-strand synthesis primer was then
 restricted by digestion with XhoI from Promega (40U/ul); all
 XhoI sites in the cDNA would be protected by their
 hemimethylated status. The cDNA constructs were
 size-fractionated with a 500 bp cutoff, using GibcoBRL Life
 Technologies' cDNA Size Fractionation column. The column
 eluent was then precipitated, redissolved, and ligated into
 Stratagene's pBluescript II XR Predigested vector
 (pBluescript II SK(+)) vector that has been digested with
 EcoRI and XhoI, and phosphorylated by Stratagene). 100% of
 the white and blue colonies appear to contain recombinant
 plasmids with cDNA inserts, based on size (n=24 and 6,
 respectively). This library was constructed by Dr. Paul Keim
 and Dr. Virginia Coryell.

SUBMITTER

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Tel: 314 286 1800
Fax: 314 286 1810
E-mail: est@watson.wustl.edu

CITATIONS

Title: Public Soybean EST Project
Authors: Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin
,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising
,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M.,
Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T.,
Jackson,Y., Cardenas,M., McCann,R., Waterston,R., Wilson,R.
Year: 1999
Status: Unpublished

MAP DATA

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IDENTIFIERS

dbEST Id: 37082
EST name: RICR0106A
GenBank Acc: D23767
GenBank gi: 427634

CLONE INFO

Clone Id: R0106_1A
DNA type: cDNA

PRIMERS

PolyA Tail: Unknown

SEQUENCE

GCCTATCAGAATACTGCGAAAAGGGTTCTGGATCCNTGACAGTGGTCTTTAAGGATTTAG
GCCCCACAGGTCTTCTACAGCACGCTGTTCTTTGAATACTTGGGTNCTTCTTATCT
ACCCCATGTCTATTACTTGCCTGTCTACAAATATTTCCGATACGAGGGAGAGCGGGTCA
TGCATCCTGTCCAGACTTACGCCATGTACTATTGGTGTTCCTACTTCAAGAGGATCA
TGGAGACGTTCTTTGTTACCCGCTTCAGCCACGCGACTTCTCCTGTATCAAATGTCTTCA
GGAAGTGTGCCTACTACTGGACCTTGGAGCTTACATTGCTTACTACTGCAACACCCGC
TTTACAACCTGTGAGTGAATTGCAGATGAAGATTNGGGTTGGATTGGGATTCTCTGCC
AAATTGCAAACTTTTATTGCCATATCCTGCTGAGGACC

Entry Created: Dec 2 1993
Last Updated: Apr 3 2002

COMMENTS

PROJECT = 'RGP'

LIBRARY

dbEST lib id: 101
Lib Name: Rice root
Organism: Oryza sativa (japonica cultivar-group)
Cultivar: Nipponbare
Description: Prepared from seedling root.

SUBMITTER

Name: Takuji Sasaki
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Address: Rice Genome Research Program, Kannondai 2-1-2, Tsukuba,
Ibaraki 305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
E-mail: tsasaki@abr.affrc.go.jp, URL: <http://rgp.dna.affrc.go.jp/>

CITATIONS

Title: Rice cDNA from root
Authors: Minobe, Y., Sasaki, T.
Year: 1995
Status: Unpublished

MAP DATA

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IDENTIFIERS

dbEST Id: 1446792
 EST name: 7472
 GenBank Acc: T44209
 GenBank gi: 2759012

CLONE INFO

Clone Id: 123K14T7
 DNA type: cDNA

PRIMERS

Sequencing: T7
 PolyA Tail: Unknown

SEQUENCE

CAAAAACAAAAGAAAATGGAATGGTGACAAGTNTTGTATATCCACCACCTCCATCGATA
 TTGCTCAATTGTATGAGCGTCGTTGGTGTAGCCGCTCTGGCCAATATCGGTGGTCTGAA
 ATCAGAGGAAAGCATCTCAAATACTCCAAATTCGGCGTATCATCATCACCACAACCA
 CAGAAGGAGCGATTTCGGCAGCATCTCTAGCAGAAATGGAATGCTTTTGCTATACACACT
 GCGNTTCTAGCCGGTGCGGTCTTCTTCTTNGNCTTACCTTCTGATGATCTCAAGGGTTC
 TTCCTTCNCAAATCCGGACTTGCCCTCCATTTTNTTCNAAGNGGGGGATTTCGGGGGGTNN
 TTTTCCAAANANAAANTACCAGGGGGGGGGGTTCCTTTNAGGCNCAGTTTTTNCCCAA
 AGGGGGGGNGTTTTTTTTTTT

Entry Created: Jan 7 1998
 Last Updated: Jan 7 1998

LIBRARY

dbEST lib id: 71
 Lib Name: Lambda-PRL2
 Organism: Arabidopsis thaliana
 Strain: var columbia
 Vector: lambda Zip-Lox
 R. Site 1: Sal
 R. Site 2: Not
 Description: Lambda PRL2 is a cDNA library derived from equal quantities
 of 4 pools of mRNA. The mRNA sources were 1) 7 day
 germinated etiolated seedlings; 2) tissue culture grown
 roots; 3) staged plants half with 24 hour light cycle, half
 on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3
 but aerial tissue (stems, flowers and siliques. The vector
 is BRL's lambda Zip-Lox. The cDNA inserts were directionally
 cloned with Sal-Not arms using oligo dT primed cDNA.

SUBMITTER

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CITATIONS

Medline UID: 95148729
 Title: Genes galore: a summary of methods for accessing results
 from large-scale partial sequencing of anonymous Arabidopsis
 cDNA clones
 Authors: Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H.,
 McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S.,
 Thomashow, M., Retzel, E., Somerville, C.
 Citation: Plant Physiol. 106: 1241-1255 1994

MAP DATA

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IDENTIFIERS

dbEST Id: 1448982
 EST name: 8703
 GenBank Acc: T45440
 GenBank gi: 2762177

CLONE INFO

Clone Id: 129022T7
 DNA type: cDNA

PRIMERS

Sequencing: T7 dye primer
 PolyA Tail: Unknown

SEQUENCE

CCCTTGTTCTCTATCTCTNTNAATTTCCTCATCTGGGTCTTCCTCGTTTGCNCCGCTTA
 AGCACCATGAAGGTACCGTCGTCTCCNGCAGCGGCAGAGAAGTCTCAAAGCTCCCCTT
 GACCTCCCCGATTTCGGCGACTGTNGCTGATCTGCAAGANGCGTTTCATAAGANAGCTAAG
 AAGTTTACCCGTCGAGGCAAAGACTGACTCTTCCNGTGACTCCTGGNTCGANGGACAAA
 CCTGTGTCCTCAATAGCAAGAAATCACTGAAGGAGTACTGTNATGGAACAACAACCTTC
 TTAAGTGTAGTCTTCAAAGNCCTGGGGGCACAAGGTTTCTACCGGAACANTTTTCTTTC
 TTCGNGTATCTTGGGCCCT

Entry Created: Jan 9 1998
 Last Updated: Aug 4 1998

LIBRARY

dbEST lib id: 71
 Lib Name: Lambda-PRL2
 Organism: Arabidopsis thaliana
 Strain: var columbia
 Vector: lambda Zip-Lox
 R. Site 1: Sal
 R. Site 2: Not

Description: Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA.

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 Fax: 517-353-9168
 E-mail: 22313tcn@ibm.cl.msu.edu

CITATIONS

Medline UID: 95148729
 Title: Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones
 Authors: Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E., Somerville, C.
 Citation: Plant Physiol. 106: 1241-1255 1994

MAP DATA

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